

# SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNITS,  
K+betaM4 and K+betaM5

<130> D0115NP

<150> US 60/272,190

<151> 2001-02-28

<150> US 60/274,258

<151> 2001-03-07

<160> 98

<170> PatentIn version 3.0

<210> 1

<211> 1839

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (5)..(1057)

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Met Thr Gly Ser His Asp Val Ile Gly Gly Ala Gly Lys Gln Val	
1 5 10 15	

ctc tgc tgc ttt tgc aag cag aga aat aag agt ttg ggc acc tac cca	97
Leu Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro	
20 25 30	

ggg gtc cca ggg aat gcc ctg tgg ctc ctg acc tcc ccc gcc tgt aat	145
Gly Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn	
35 40 45	

gct ctg agc act tca gca gta atg cat gga aga gat aag ggg tct gtg	193
Ala Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val	
50 55 60	

acc cat gga act gtc caa gtc ctc tct gac acc cgc ttc ttt tcc tgc	241
Thr His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys	
65 70 75	

cgt gaa gga cta ctt cca gca acc cag tct cct gcc atg tcc gac ccc	289
Arg Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro	
80 85 90 95	

atc acg ctg aac gtc ggg ggg aag ctc tat aca acc tca ctg gcg acc	337
Ile Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr	
100 105 110	

ctg acc agc ttc cct gac tcc atg cta ggc gcc atg ttc agc ggg aag	385
Leu Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys	
115 120 125	
atg ccc acc aag agg gac agc cag ggc aac tgc ttc att gac cgt gac	433
Met Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp	
130 135 140	
ggc aaa gtg ttc cgc tat atc ctc aac ttc ctg cgg acc tcc cac ctt	481
Gly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu	
145 150 155	
gac ctg cct gag gac ttc cag gag atg ggg ctg ctc cgc agg gag gcc	529
Asp Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala	
160 165 170 175	
gac ttc tac cag gtg cag ccc ctg att gag gcc ctg cag gag aag gaa	577
Asp Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu	
180 185 190	
gtg gag ctc tcc aag gcc gag aag aat gcc atg ctc aac atc aca ctg	625
Val Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu	
195 200 205	
aac cag cgt gtg cag acg gtc cac ttc act gtg cgc gag gca ccc cag	673
Asn Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln	
210 215 220	
atc tac agc ctc tcc tct tcc agc atg gag gtc ttc aac gcc aac atc	721
Ile Tyr Ser Leu Ser Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile	
225 230 235	
ttc agc acc tcc tgc ctc ttc ctc aag ctc ctt ggc tct aag ctc ttc	769
Phe Ser Thr Ser Cys Leu Phe Leu Lys Leu Gly Ser Lys Leu Phe	
240 245 250 255	
tac tgc tcc aat ggc aat ctc tcc tcc atc acc agc cac ttg cag gac	817
Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp	
260 265 270	
ccc aac cac ctg act ctg gac tgg gtg gcc aat gtg gag ggc ctg cca	865
Pro Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro	
275 280 285	
gag gag gag tac acc aag cag aac ctc aag agg ctc tgg gtg gtg ccc	913
Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro	
290 295 300	
gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg	961
Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu	
305 310 315	
aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat	1009
Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His	
320 325 330 335	
gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg	1057

Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg  
340 345 350

taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117  
ttggagggca tctgccaggt ggtgcgaggc aggggactat actaatctgt attaattgtg 1177  
tagcaggact tgattccccc catgatgaag tccacctttt ggaatccagt gtcctctgaa 1237  
cagaaccacc ttttttcttg ccattttgag ctgcagacag gcggtttatt atgacaagtg 1297  
aagagtcagc tgatgtgtac taaaggaggc cataggagga ttttccagcc aggacaaaag 1357  
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atctgtaaga aggccctggg ggagaggatg ggatgagaac aagaggctac ctccagttaa 1477  
ccaggacata aagtccccag cggttcctgt cacacctgct cctccctccc cagggtgcat 1537  
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gaggaatgag tgtccaggca gagttcagaa ggtaggaatg tccctcttga tagggctgaa 1717  
tcaagggatt cctggcttta gaaaggggtct gctatctttg caaaaatgtg caagtatctg 1777  
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aa 1839

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<212> PRT  
<213> homo sapiens

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Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro Gly  
20 25 30

Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn Ala  
35 40 45

Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val Thr  
50 55 60

His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys Arg  
65 70 75 80

Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro Ile  
                     85                    90                    95

Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr Leu  
                     100                    105                    110

Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys Met  
                     115                    120                    125

Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp Gly  
                     130                    135                    140

Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu Asp  
 145                    150                    155                    160

Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala Asp  
                     165                    170                    175

Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu Val  
                     180                    185                    190

Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu Asn  
                     195                    200                    205

Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln Ile  
                     210                    215                    220

Tyr Ser Leu Ser Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile Phe  
 225                    230                    235                    240

Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe Tyr  
                     245                    250                    255

Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp Pro  
                     260                    265                    270

Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro Glu  
                     275                    280                    285

Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro Ala  
                     290                    295                    300

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Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu Lys  
 305 310 315 320

Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His Ala  
 325 330 335

Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg  
 340 345 350

<210> 3  
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 <212> PRT  
 <213> homo sapiens

<400> 3

Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu  
 1 5 10 15

Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg  
 20 25 30

Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr  
 35 40 45

Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu  
 50 55 60

Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro  
 65 70 75 80

Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr  
 85 90 95

Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr  
 100 105 110

Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys  
 115 120 125

Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr  
 130 135 140

Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe  
 145 150 155 160

Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser  
 165 170 175

Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val  
 180 185 190

~~His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr~~

195                                      200                                      205  
 Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His  
 210                                      215                                      220  
 Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp  
 225                                      230                                      235  
  
 <210> 4  
 <211> 256  
 <212> PRT  
 <213> homo sapiens  
  
 <220>  
 <221> UNSURE  
 <222> (15)..(15)  
 <223> wherein "X" is equal to any amino acid.  
  
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 Met Ser Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Xaa Asn  
 1                                      5                                      10                                      15  
 Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val  
 20                                      25                                      30  
 His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu  
 35                                      40                                      45  
 Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu  
 50                                      55                                      60  
 Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp  
 65                                      70                                      75                                      80  
 Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu  
 85                                      90                                      95  
 Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala  
 100                                      105                                      110  
 Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys  
 115                                      120                                      125  
 Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val  
 130                                      135                                      140  
 Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp  
 145                                      150                                      155                                      160  
 Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys  
 165                                      170                                      175  
 Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg  
 180                                      185                                      190

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Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu  
195 200 205

Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly  
210 215 220

Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg  
225 230 235 240

Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu  
245 250 255

<210> 5

<211> 234

<212> PRT

<213> homo sapiens

<400> 5

Met Pro His Arg Lys Glu Arg Pro Ser Gly Ser Ser Leu His Thr His  
1 5 10 15

Gly Ser Thr Gly Thr Ala Glu Gly Gly Asn Met Ser Arg Leu Ser Leu  
20 25 30

Thr Arg Ser Pro Val Ser Pro Leu Ala Ala Gln Gly Ile Pro Leu Pro  
35 40 45

Ala Gln Leu Thr Lys Ser Asn Ala Pro Val His Ile Asp Val Gly Ser  
50 55 60

His Met Tyr Thr Ser Ser Leu Ala Thr Leu Thr Lys Tyr Pro Asp Ser  
65 70 75 80

Arg Ile Ser Arg Leu Phe Asn Gly Thr Glu Pro Ile Val Leu Asp Ser  
85 90 95

Leu Lys Gln His Tyr Phe Ile Asp Arg Asp Gly Glu Ile Phe Arg Tyr  
100 105 110

Val Leu Ser Phe Leu Arg Thr Ser Lys Leu Leu Leu Pro Asp Asp Phe  
115 120 125

Lys Asp Phe Ser Leu Leu Tyr Glu Glu Ala Arg Tyr Tyr Gln Leu Gln  
130 135 140

Pro Met Val Arg Glu Leu Glu Arg Trp Gln Gln Glu Gln Glu Gln Arg  
145 150 155 160

Arg Arg Ser Arg Ala Cys Asp Cys Leu Val Val Arg Val Thr Pro Asp  
165 170 175

Leu Gly Glu Arg Ile Ala Leu Ser Gly Glu Lys Ala Leu Ile Glu Glu  
180 185 190

Val Phe Pro Glu Thr Gly Asp Val Met Cys Asn Ser Val Asn Ala Gly  
195 200 205

Trp Asn Gln Asp Pro Thr His Val Ile Arg Phe Pro Leu Asn Gly Tyr  
 210 215 220

Cys Arg Leu Asn Ser Val Gln Asp Val Leu  
 225 230

<210> 6

<211> 338

<212> PRT

<213> Drosophila melanogaster

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Met Asp Arg Glu Arg Glu Arg Asp Val Lys Ala Leu Glu Pro Arg Asp  
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Leu Ser Ser Thr Gly Arg Ile Tyr Ala Arg Ser Asp Ile Lys Ile Ser  
 20 25 30

Ser Ser Pro Thr Val Ser Pro Thr Ile Ser Asn Ser Ser Ser Pro Thr  
 35 40 45

Pro Thr Pro Pro Ala Ser Ser Ser Val Thr Pro Leu Gly Leu Pro Gly  
 50 55 60

Ala Val Ala Ala Ala Ala Ala Ala Val Gly Gly Ala Ser Ser Ala Gly  
 65 70 75 80

Ala Ser Ser Tyr Leu His Gly Asn His Lys Pro Ile Thr Gly Ile Pro  
 85 90 95

Cys Val Ala Ala Ala Ser Arg Tyr Thr Ala Pro Val His Ile Asp Val  
 100 105 110

Gly Gly Thr Ile Tyr Thr Ser Ser Leu Glu Thr Leu Thr Lys Tyr Pro  
 115 120 125

Glu Ser Lys Leu Ala Lys Leu Phe Asn Gly Gln Ile Pro Ile Val Leu  
 130 135 140

Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp Gly Gly Met Phe  
 145 150 155 160

Arg His Ile Leu Asn Phe Met Arg Asn Ser Arg Leu Leu Ile Ala Glu  
 165 170 175

Asp Phe Pro Asp Leu Glu Leu Leu Leu Glu Glu Ala Arg Tyr Tyr Glu  
 180 185 190

Val Glu Pro Met Ile Lys Gln Leu Glu Ser Met Arg Lys Asp Arg Val  
 195 200 205

Arg Asn Gly Asn Tyr Leu Val Ala Pro Pro Thr Pro Pro Ala Arg His  
 210 215 220

~~Ile Lys Thr Ser Pro Arg Thr Ser Ala Ser Pro Glu Cys Asn Tyr Glu~~



225                      230                      235                      240  
 Val Val Ala Leu His Ile Ser Pro Asp Leu Gly Glu Arg Ile Met Leu  
                                  245                      250                      255  
 Ser Ala Glu Arg Ala Leu Leu Asp Glu Leu Phe Pro Glu Ala Ser Gln  
                                  260                      265                      270  
 Ala Thr Gln Ser Ser Arg Ser Gly Val Ser Trp Asn Gln Gly Asp Trp  
                                  275                      280                      285  
 Gly Gln Ile Ile Arg Phe Pro Leu Asn Gly Tyr Cys Lys Leu Asn Ser  
                                  290                      295                      300  
 Val Gln Val Leu Thr Arg Leu Leu Asn Ala Gly Phe Thr Ile Glu Ala  
 305                                   310                      315                      320  
 Ser Val Gly Gly Gln Gln Phe Ser Glu Tyr Leu Leu Ala Arg Arg Val  
                                  325                      330                      335

Pro Met

<210> 7  
 <211> 733  
 <212> DNA  
 <213> homo sapiens

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 aattcgaggg tgcaccgtca gtcttctct tcccccaaa acccaaggac accctcatga 120  
 tctcccgga tcttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180  
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240  
 aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300  
 ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca acccccatcg 360  
 agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420  
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct 480  
 atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC aactacaaga 540  
 ccacgcctcc cgtgctggac tccgacggct ctttcttct ctacagcaag ctacccgtgg 600  
 acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660  
 acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720  
 gactctagag gat 733

<210> 8

<211> 724  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> Unsure  
 <222> (1)..(3)  
 <223> wherein "N" is equal to "A", "G", "C", or "T".

<400> 8  
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 aattcatttc gatcccaagg gcataggctt gatgtacaat aaggagttaa ggactgttaa 120  
 ttctctgata aggttttggt atagtcattt ctcaattctc accctctcca ggactacttc 180  
 cagcaaccca gtctcctgcc atgtccgacc ccatcacgct gaacgtcggg gggaagctct 240  
 atacaacctc actggcgacc ctgaccagct tccctgactc catgctagge gccatgttca 300  
 gcgggaagat gccaccaag agggacagcc agggcaactg cttcattgac cgtgacggca 360  
 aagtgttccg ctatatctc aacttcctgc ggacctcca cttgacctg cctgaggact 420  
 tccaggagat ggggctgctc cgcaggagg cgcacttcta ccagggtgcag cccctgattg 480  
 aggccttgca ggagaaggaa gtggagctct ccaaggccga gaagaatgcc atgctcaaca 540  
 tcacactgaa ccagcgtgtg cagacgggtcc acttcactgt gcgcgaggca cccagatct 600  
 acagcctctc ctcttcacgc atggaggtct tcaacgcaa catcttcage acctcctgcc 660  
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 tcac 724

<210> 9  
 <211> 74  
 <212> DNA  
 <213> homo sapiens

<400> 9  
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 ctcttggtgg gcat 74

<210> 10  
 <211> 20  
 <212> DNA  
 <213> homo sapiens

<400> 10  
 atacaacctc actggcgacc 20

<210> 11  
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 <212> DNA  
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<400> 11  
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20

<210> 12  
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<400> 12

Asp Pro Ile Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu  
 1 5 10 15

Ala Thr Leu Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser  
 20 25 30

Gly Lys Met Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp  
 35 40 45

Arg Asp Gly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser  
 50 55 60

His Leu Asp Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg  
 65 70 75 80

Glu Ala Asp Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu  
 85 90 95

Lys Glu Val

<210> 13  
 <211> 14  
 <212> PRT  
 <213> homo sapiens

<400> 13

Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro Gly  
 1 5 10

<210> 14  
 <211> 14  
 <212> PRT  
 <213> homo sapiens

<400> 14

Lys Asn Ala Met Leu Asn Ile Thr Leu Asn Gln Arg Val Gln  
 1 5 10

<210> 15  
<211> 14  
<212> PRT  
<213> homo sapiens

<400> 15

Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu  
1 5 10

<210> 16  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 16

Asp Thr Arg Phe Phe Ser Cys Arg Glu Gly Leu Leu Pro  
1 5 10

<210> 17  
<211> 13  
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<400> 17

Leu Gly Ala Met Phe Ser Gly Lys Met Pro Thr Lys Arg  
1 5 10

<210> 18  
<211> 13  
<212> PRT  
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<400> 18

Ser Gly Lys Met Pro Thr Lys Arg Asp Ser Gln Gly Asn  
1 5 10

<210> 19  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 19

Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln Ile  
1 5 10

<210> 20  
<211> 26  
<212> PRT  
<213> homo sapiens

<400> 20

Gly Thr Tyr Pro Gly Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser  
 1 5 10 15

Pro Ala Cys Asn Ala Leu Ser Thr Ser Ala  
 20 25

<210> 21  
 <211> 25  
 <212> PRT  
 <213> homo sapiens

<400> 21

Val Phe Asn Ala Asn Ile Phe Ser Thr Ser Cys Leu Phe Leu Lys Leu  
 1 5 10 15

Leu Gly Ser Lys Leu Phe Tyr Cys Ser  
 20 25

<210> 22  
 <211> 8  
 <212> PRT  
 <213> bacteriophage T7

<400> 22

Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 23  
 <211> 2154  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1029)

<400> 23

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 Met Thr Met Ala Val Leu Arg Asn Arg Lys Gly Gly Lys Gly Pro Leu  
 1 5 10 15

agg cgc cgg ccg ctg gcg ctg cct gct ctt cga ctg ggc gag ctt cct 96  
 Arg Arg Arg Pro Leu Ala Leu Pro Ala Leu Arg Leu Gly Glu Leu Pro  
 20 25 30

gcc aat cag ggc gga acc agc gcg gcg tcg gcc agt agc ggg agg cgg 144  
 Ala Asn Gln Gly Gly Thr Ser Ala Ala Ser Ala Ser Ser Gly Arg Arg  
 35 40 45

tcg ggt cag gcc cca gct ggg cgc gag cgg gtc ggc gtt gag gga gcc 192  
 Ser Gly Gln Ala Pro Ala Gly Arg Glu Arg Val Gly Val Glu Gly Ala  
 50 55 60

-----acc-gcc-ctc-ccg-cct-geg-cac-tgc-ctc-tcg-ccc-ccc-tcc-ggc-cag-ccc----- 240

Thr	Ala	Leu	Pro	Pro	Ala	His	Cys	Leu	Ser	Pro	Pro	Ser	Gly	Gln	Pro	
65					70					75					80	
gca	gcc	ggc	cgc	gtc	atg	cca	ggc	gct	gct	cgg	cga	gcc	aga	ggg	atg	288
Ala	Ala	Gly	Arg	Val	Met	Pro	Gly	Ala	Ala	Arg	Arg	Ala	Arg	Gly	Met	
				85					90					95		
gtg	gta	gtc	acg	ggg	cgg	gag	cca	gac	agc	cgt	cgt	cag	gac	ggg	gcc	336
Val	Val	Val	Thr	Gly	Arg	Glu	Pro	Asp	Ser	Arg	Arg	Gln	Asp	Gly	Ala	
			100					105					110			
atg	tcc	agc	tct	gac	gcc	gaa	gac	gac	ttt	ctg	gag	cgc	gcc	acg	cgc	384
Met	Ser	Ser	Ser	Asp	Ala	Glu	Asp	Asp	Phe	Leu	Glu	Pro	Ala	Thr	Pro	
		115					120					125				
acg	gcc	acg	cag	gcg	ggg	cac	gcg	ctg	ccc	ctg	ctg	cca	cag	gag	ttt	432
Thr	Ala	Thr	Gln	Ala	Gly	His	Ala	Leu	Pro	Leu	Leu	Pro	Gln	Glu	Phe	
	130					135				140						
cct	gag	gtt	gtt	ccc	ctt	aac	atc	gga	ggg	gct	cac	ttc	act	aca	cgc	480
Pro	Glu	Val	Val	Pro	Leu	Asn	Ile	Gly	Gly	Ala	His	Phe	Thr	Thr	Arg	
145					150				155						160	
ctg	tcc	aca	ctg	cgg	tgc	tac	gaa	gac	acc	atg	ttg	gca	gcc	atg	ttc	528
Leu	Ser	Thr	Leu	Arg	Cys	Tyr	Glu	Asp	Thr	Met	Leu	Ala	Ala	Met	Phe	
				165					170					175		
agt	ggg	cgg	cac	tac	atc	ccc	aca	gac	tcc	gag	ggc	cgg	tac	ttc	atc	576
Ser	Gly	Arg	His	Tyr	Ile	Pro	Thr	Asp	Ser	Glu	Gly	Arg	Tyr	Phe	Ile	
			180					185					190			
gac	cga	gat	ggc	aca	cac	ttt	gga	gat	gtg	ctg	aat	ttc	ctg	cgc	tca	624
Asp	Arg	Asp	Gly	Thr	His	Phe	Gly	Asp	Val	Leu	Asn	Phe	Leu	Arg	Ser	
		195					200					205				
ggg	gac	ctc	cca	ccc	agg	gag	cgt	gtt	cga	gct	gtg	tac	aaa	gag	gcc	672
Gly	Asp	Leu	Pro	Pro	Arg	Glu	Arg	Val	Arg	Ala	Val	Tyr	Lys	Glu	Ala	
	210					215					220					
cag	tac	tat	gcc	atc	ggg	ccc	ctc	ctg	gag	cag	ctg	gag	aac	atg	cag	720
Gln	Tyr	Tyr	Ala	Ile	Gly	Pro	Leu	Leu	Glu	Gln	Leu	Glu	Asn	Met	Gln	
225					230					235					240	
cca	ctg	aag	ggc	gag	aag	gtg	cgc	caa	gcg	ttt	ctg	gga	ctc	atg	ccc	768
Pro	Leu	Lys	Gly	Glu	Lys	Val	Arg	Gln	Ala	Phe	Leu	Gly	Leu	Met	Pro	
				245					250					255		
tat	tac	aaa	gac	cac	ttg	gag	cgg	att	gtg	gag	atc	gcc	cgg	ctg	cgt	816
Tyr	Tyr	Lys	Asp	His	Leu	Glu	Arg	Ile	Val	Glu	Ile	Ala	Arg	Leu	Arg	
			260					265					270			
gcg	gtc	cag	cgg	aag	gcc	cgc	ttt	gcc	aag	ctc	aag	agc	ttg	aca	cct	864
Ala	Val	Gln	Arg	Lys	Ala	Arg	Phe	Ala	Lys	Leu	Lys	Ser	Leu	Thr	Pro	
		275					280					285				
tcc	tgg	cta	atg	agt	gtc	ctc	atc	aag	atg	ccc	cct	gga	gtc	aca	tca	912
<del>Ser</del>	<del>Trp</del>	<del>Leu</del>	<del>Met</del>	<del>Ser</del>	<del>Val</del>	<del>Leu</del>	<del>Ile</del>	<del>Lys</del>	<del>Met</del>	<del>Pro</del>	<del>Pro</del>	<del>Gly</del>	<del>Val</del>	<del>Thr</del>	<del>Ser</del>	

290	295	300	
tgg att aac gca gaa agg cgg ctg tat ttg gaa act ccc att ggt cca			960
Trp Ile Asn Ala Glu Arg Arg Leu Tyr Leu Glu Thr Pro Ile Gly Pro			
305	310	315	320
gag aga cag aac aat gag aag aaa tcc cct gtc cag ttg cct gca gga			1008
Glu Arg Gln Asn Asn Glu Lys Lys Ser Pro Val Gln Leu Pro Ala Gly			
325	330	335	
gta ttc caa cac ttc atg ggc tagaggattc cattgagatg gggtttacgt			1059
Val Phe Gln His Phe Met Gly			
340			
cttgattttg aacacctgtc agcactgttc tctgtttgca tggcaattct gaccctttta			1119
tggcaacaac acccctggga caaccagat ttgtagattg agatccaaag gtagaatttc			1179
cagacagtcc aaccaaggta tcaagtgatg tttccagagt ggaaggctct caccgtgtcc			1239
caggatttct ggggtttgta agcagtactg gccatttgtg accctgtttt ttacctaatc			1299
attctgtctt tttaggacat ggttttaccc gatccctggc aaaggatcca gaattccaat			1359
agctgaaaac cctgttatag cttttctcct attctgcctt acccaagaca cacttgaacc			1419
cctcagtaag gctatagaga gggccatgag caggggcagc ctctcccttg tttctacagc			1479
tccatgatga ggggttgact gagggcagca atccttgtag gtgtgacagt tgcaatataa			1539
ttaacagttt caagatctag aggtaccttt tgaaagaacc ccttcaggga tatctatcca			1599
cagtagcctg gagcagccaa ggtgaacctg agattttgac ccacacaata agggggggcc			1659
attctttttc aaatatatttg gcttcagaat acacttcatt acacatgcaa atattgagag			1719
attaacagaa attccagctc ttatgcctaa ctgagaagag ccaactgcaag ttgcagttag			1779
gtacccatgt gcagcagagg ccagctgaat ccagagctt cccaaagtgg acaccagcgg			1839
ggactattcc tgatgtccca cccaagagag gaagatgagc tgaggcgctc ttgctctgcc			1899
caaatgcac ccatgtgcat tcacgtgtca cccattcaaa ataacatggc attcttggaa			1959
ccttgatatc gacatgtaag accagcctac acattggggg gggcgcagg gctcacactt			2019
gtaatcctag cactttggaa ggctgaggtg ggcagattgc ttgagcacag gagttccaga			2079
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aaaaaaaaa aaaaa			2154

<210> 24

<211> 343

<212> PRT

<213> homo sapiens

<400> 24

Met Thr Met Ala Val Leu Arg Asn Arg Lys Gly Gly Lys Gly Pro Leu  
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Arg Arg Arg Pro Leu Ala Leu Pro Ala Leu Arg Leu Gly Glu Leu Pro  
20 25 30

Ala Asn Gln Gly Gly Thr Ser Ala Ala Ser Ala Ser Ser Gly Arg Arg  
35 40 45

Ser Gly Gln Ala Pro Ala Gly Arg Glu Arg Val Gly Val Glu Gly Ala  
50 55 60

Thr Ala Leu Pro Pro Ala His Cys Leu Ser Pro Pro Ser Gly Gln Pro  
65 70 75 80

Ala Ala Gly Arg Val Met Pro Gly Ala Ala Arg Arg Ala Arg Gly Met  
85 90 95

Val Val Val Thr Gly Arg Glu Pro Asp Ser Arg Arg Gln Asp Gly Ala  
100 105 110

Met Ser Ser Ser Asp Ala Glu Asp Asp Phe Leu Glu Pro Ala Thr Pro  
115 120 125

Thr Ala Thr Gln Ala Gly His Ala Leu Pro Leu Leu Pro Gln Glu Phe  
130 135 140

Pro Glu Val Val Pro Leu Asn Ile Gly Gly Ala His Phe Thr Thr Arg  
145 150 155 160

Leu Ser Thr Leu Arg Cys Tyr Glu Asp Thr Met Leu Ala Ala Met Phe  
165 170 175

Ser Gly Arg His Tyr Ile Pro Thr Asp Ser Glu Gly Arg Tyr Phe Ile  
180 185 190

Asp Arg Asp Gly Thr His Phe Gly Asp Val Leu Asn Phe Leu Arg Ser  
195 200 205

Gly Asp Leu Pro Pro Arg Glu Arg Val Arg Ala Val Tyr Lys Glu Ala  
210 215 220



Gln Tyr Tyr Ala Ile Gly Pro Leu Leu Glu Gln Leu Glu Asn Met Gln  
225 230 235 240

Pro Leu Lys Gly Glu Lys Val Arg Gln Ala Phe Leu Gly Leu Met Pro  
245 250 255

Tyr Tyr Lys Asp His Leu Glu Arg Ile Val Glu Ile Ala Arg Leu Arg  
260 265 270

Ala Val Gln Arg Lys Ala Arg Phe Ala Lys Leu Lys Ser Leu Thr Pro  
275 280 285

Ser Trp Leu Met Ser Val Leu Ile Lys Met Pro Pro Gly Val Thr Ser  
290 295 300

Trp Ile Asn Ala Glu Arg Arg Leu Tyr Leu Glu Thr Pro Ile Gly Pro  
305 310 315 320

Glu Arg Gln Asn Asn Glu Lys Lys Ser Pro Val Gln Leu Pro Ala Gly  
325 330 335

Val Phe Gln His Phe Met Gly  
340

<210> 25  
<211> 225  
<212> PRT  
<213> homo sapiens

<400> 25

Met Ser Thr Val Val Glu Leu Asn Val Gly Gly Glu Phe His Thr Thr  
1 5 10 15

Thr Leu Gly Thr Leu Arg Lys Phe Pro Gly Ser Lys Leu Ala Glu Met  
20 25 30

Phe Ser Ser Leu Ala Lys Ala Ser Thr Asp Ala Glu Gly Arg Phe Phe  
35 40 45

Ile Asp Arg Pro Ser Thr Tyr Phe Arg Pro Ile Leu Asp Tyr Leu Arg  
50 55 60

Thr Gly Gln Val Pro Thr Gln His Ile Pro Glu Val Tyr Arg Glu Ala  
65 70 75 80

-----Gln-Phe-Tyr-Glu-Ile-Lys-Pro-Leu-Val-Lys-Leu-Leu-Glu-Asp-Met-Pro-----

85					90					95					
Gln	Ile	Phe	Gly	Glu	Gln	Val	Ser	Arg	Lys	Gln	Phe	Leu	Leu	Gln	Val
			100					105					110		
Pro	Gly	Tyr	Ser	Glu	Asn	Leu	Glu	Leu	Met	Val	Arg	Leu	Ala	Arg	Ala
		115					120					125			
Glu	Ala	Ile	Thr	Ala	Arg	Lys	Ser	Ser	Val	Leu	Val	Cys	Leu	Val	Glu
	130					135					140				
Thr	Glu	Glu	Gln	Asp	Ala	Tyr	Tyr	Ser	Glu	Val	Leu	Cys	Phe	Leu	Gln
	145					150					155				160
Asp	Lys	Lys	Met	Phe	Lys	Ser	Val	Val	Lys	Phe	Gly	Pro	Trp	Lys	Ala
				165					170					175	
Val	Leu	Asp	Asn	Ser	Asp	Leu	Met	His	Cys	Leu	Glu	Met	Asp	Ile	Lys
			180					185					190		
Ala	Gln	Gly	Tyr	Lys	Val	Phe	Ser	Lys	Phe	Tyr	Leu	Thr	Tyr	Pro	Thr
		195					200					205			
Lys	Arg	Asn	Glu	Phe	His	Phe	Asn	Ile	Tyr	Ser	Phe	Thr	Phe	Thr	Trp
	210					215					220				

Trp  
225

<210> 26  
 <211> 313  
 <212> PRT  
 <213> homo sapiens

<400> 26

Met	Glu	Glu	Met	Ser	Gly	Glu	Ser	Val	Val	Ser	Ser	Ala	Val	Pro	Ala
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Ala	Ala	Thr	Arg	Thr	Thr	Ser	Phe	Lys	Gly	Thr	Ser	Pro	Ser	Ser	Lys
			20					25					30		
Tyr	Val	Lys	Leu	Asn	Val	Gly	Gly	Ala	Leu	Tyr	Tyr	Thr	Thr	Met	Gln
		35					40					45			
Thr	Leu	Thr	Lys	Gln	Asp	Thr	Met	Leu	Lys	Ala	Met	Phe	Ser	Gly	Arg
	50					55					60				
Met	Glu	Val	Leu	Thr	Asp	Ser	Glu	Gly	Trp	Ile	Leu	Ile	Asp	Arg	Cys
65					70					75					80
Gly	Lys	His	Phe	Gly	Thr	Ile	Leu	Asn	Tyr	Leu	Arg	Asp	Gly	Ala	Val
				85					90					95	
Pro	Leu	Pro	Glu	Ser	Arg	Arg	Glu	Ile	Glu	Glu	Leu	Leu	Ala	Glu	Ala
			100					105						110	

Lys Tyr Tyr Leu Val Gln Gly Leu Val Glu Glu Cys Gln Ala Ala Leu  
 115 120 125  
 Gln Asn Lys Asp Thr Tyr Glu Pro Phe Cys Lys Val Pro Val Ile Thr  
 130 135 140  
 Ser Ser Lys Glu Glu Gln Lys Leu Ile Ala Thr Ser Asn Lys Pro Ala  
 145 150 155 160  
 Val Lys Leu Leu Tyr Asn Arg Ser Asn Asn Lys Tyr Ser Tyr Thr Ser  
 165 170 175  
 Asn Ser Asp Asp Asn Met Leu Lys Asn Ile Glu Leu Phe Asp Lys Leu  
 180 185 190  
 Ser Leu Arg Phe Asn Gly Arg Val Leu Phe Ile Lys Asp Val Ile Gly  
 195 200 205  
 Asp Glu Ile Cys Cys Trp Ser Phe Tyr Gly Gln Gly Arg Lys Ile Ala  
 210 215 220  
 Glu Val Cys Cys Thr Ser Ile Val Tyr Ala Thr Glu Lys Lys Gln Thr  
 225 230 235 240  
 Lys Val Glu Phe Pro Glu Ala Arg Ile Tyr Glu Glu Thr Leu Asn Ile  
 245 250 255  
 Leu Leu Tyr Glu Ala Gln Asp Gly Arg Gly Pro Asp Asn Ala Leu Leu  
 260 265 270  
 Glu Ala Thr Gly Gly Ala Ala Gly Arg Ser His His Leu Asp Glu Asp  
 275 280 285  
 Glu Glu Arg Glu Arg Ile Glu Arg Val Arg Arg Ile His Ile Lys Arg  
 290 295 300  
 Pro Asp Asp Arg Ala His Leu His Gln  
 305 310

<210> 27  
 <211> 301  
 <212> PRT  
 <213> Drosophila melanogaster

<400> 27

Met Ser Glu Ser Met Ser Gly Asp His Lys Ile Leu Leu Lys Gly His  
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 Ser Ser Gln Tyr Leu Lys Leu Asn Val Gly Gly His Leu Tyr Tyr Thr  
 20 25 30  
 Thr Ile Gly Thr Leu Thr Lys Asn Asn Asp Thr Met Leu Ser Ala Met  
 35 40 45  
 Phe Ser Gly Arg Met Glu Val Leu Thr Asp Ser Glu Gly Trp Ile Leu  
 50 55 60

Ile Asp Arg Cys Gly Asn His Phe Gly Ile Ile Leu Asn Tyr Leu Arg  
 65 70 75 80  
 Asp Gly Thr Val Pro Leu Pro Glu Thr Asn Lys Glu Ile Ala Glu Leu  
 85 90 95  
 Leu Ala Glu Ala Lys Tyr Tyr Cys Ile Thr Glu Leu Ala Ile Ser Cys  
 100 105 110  
 Glu Arg Ala Leu Tyr Ala His Gln Glu Pro Lys Pro Ile Cys Arg Ile  
 115 120 125  
 Pro Leu Ile Thr Ser Gln Lys Glu Glu Gln Leu Leu Leu Ser Val Ser  
 130 135 140  
 Leu Lys Pro Ala Val Ile Leu Val Val Gln Arg Gln Asn Asn Lys Tyr  
 145 150 155 160  
 Ser Tyr Thr Ser Thr Ser Asp Asp Asn Leu Leu Lys Asn Ile Glu Leu  
 165 170 175  
 Phe Asp Lys Leu Ser Leu Arg Phe Asn Glu Arg Ile Leu Phe Ile Lys  
 180 185 190  
 Asp Val Ile Gly Pro Ser Glu Ile Cys Cys Trp Ser Phe Tyr Gly His  
 195 200 205  
 Gly Lys Lys Val Ala Glu Val Cys Cys Thr Ser Ile Val Tyr Ala Thr  
 210 215 220  
 Asp Arg Lys His Thr Lys Val Glu Phe Pro Glu Ala Arg Ile Tyr Glu  
 225 230 235 240  
 Glu Thr Leu Gln Val Leu Leu Tyr Glu Asn Arg Asn Ala Pro Asp Gln  
 245 250 255  
 Glu Leu Met Gln Ala Thr Ser Ser Ala Arg Val Gly Ser Ala Ser Gly  
 260 265 270  
 Thr Ser Ile Asn Gln Tyr Thr Ser Asp Glu Glu Glu Glu Arg Thr Gly  
 275 280 285  
 Leu Ala Arg Leu Arg Ser Asn Lys Arg Asn Asn Pro Ser  
 290 295 300

<210> 28  
 <211> 221  
 <212> PRT  
 <213> Caenorhabditis elegans

<400> 28

Met Glu Pro Ser Thr Ile Val Lys Leu Asp Val Gly Gly Lys Ile Phe  
 1 5 10 15

~~Lys Thr Thr Ile Phe Thr Leu Cys Lys His Asp Ser Met Leu Lys Thr~~

20					25					30					
Met	Phe	Cys	Thr	Asp	Val	Pro	Val	Thr	Lys	Asn	Glu	Glu	Gly	Ser	Val
		35					40					45			
Phe	Ile	Asp	Arg	Asp	Ser	Lys	His	Phe	Arg	Leu	Ile	Leu	Asn	Phe	Leu
	50					55					60				
Arg	Asp	Gly	Gln	Ile	Ala	Leu	Pro	Asp	Ser	Asp	Arg	Glu	Val	Arg	Glu
65					70				75						80
Val	Leu	Ala	Glu	Ala	Ser	Tyr	Phe	Leu	Leu	Asp	Pro	Leu	Ile	Glu	Leu
				85					90					95	
Cys	Gly	Glu	Arg	Leu	Glu	Gln	Ser	Leu	Asn	Pro	Tyr	Tyr	His	Leu	Val
			100					105					110		
Ser	Thr	Val	Leu	Glu	Ala	Arg	Lys	Ile	Ile	Phe	Ala	Thr	Glu	Lys	Pro
		115					120					125			
Ile	Val	Val	Leu	Arg	Leu	Pro	Val	Tyr	Ile	Ala	Thr	Ser	Gly	Asn	Gln
	130					135					140				
Ser	Tyr	Tyr	Phe	Ser	Glu	Thr	Lys	Phe	Arg	Glu	Leu	Ser	Glu	Glu	Tyr
145					150					155					160
His	Lys	His	Val	Ala	Phe	Ile	Leu	Ile	Thr	Glu	Pro	Glu	Phe	Asn	Glu
				165					170					175	
Asp	Cys	Ser	Trp	Ser	Phe	Phe	Leu	Arg	Ala	Lys	Lys	Ile	Thr	Ala	Arg
			180					185					190		
Ile	Lys	Gly	Pro	Met	Asp	Cys	Asn	Leu	Val	Glu	Glu	Cys	Met	Pro	Lys
		195					200					205			
Thr	Val	Glu	Arg	Arg	Arg	Glu	Lys	Lys	Thr	Trp	His	His			
	210					215					220				

<210> 29  
 <211> 583  
 <212> DNA  
 <213> homo sapiens

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 agagaagaaa gtgttcagat ggacccgtgg gcttgagtga ctgaatgaat ggtgtggcac 120  
 caatcagacc ccagggttg aagatggagc agccccagct ctcattcccc gttgcctgcc 180  
 tgagagccct ggtgatttct ttccagtttc ctgaggttgt tccccttaac atcgagggg 240  
 ctcacttcac tacacgctg tccacactgc ggtgctacga agacaccatg ttggcagcca 300  
 tgttcagtgg gcggcactac atccccacgg actccgaggg ccggtacttc atcgaccgag 360  
 -----atggcacaca-ctttgggtat-gtctcttccct-ctacaatcaa-ctttgtagtc-ctagcagggtg----- 420

attagcgtag gcttgagtat gggaccttga tatcttccat agtacctaga agaggagata 480  
gcatattgat gaaatttaaat aaatgggttt attgaaagag atcaattttt tttttttttt 540  
ttgccaaagg agacaaagac agccagagaa attcgaaata aca 583

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<211> 80  
<212> DNA  
<213> homo sapiens

<400> 30  
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caacatgggtg ttttcgtagc 80

<210> 31  
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<213> homo sapiens

<400> 31  
tgttcccctt aacatcggag 20

<210> 32  
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<213> homo sapiens

<400> 32  
catacccaaa gtgtgtgcca 20

<210> 33  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 33

Ala Ala Ser Ala Ser Ser Gly Arg Arg Ser Gly Gln Ala  
1 5 10

<210> 34  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 34

Gly Met Val Val Val Thr Gly Arg Glu Pro Asp Ser Arg  
1 5 10

<210> 35  
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 <212> PRT  
 <213> homo sapiens

<400> 35

Gly Arg Glu Pro Asp Ser Arg Arg Gln Asp Gly Ala Met  
 1 5 10

<210> 36  
 <211> 13  
 <212> PRT  
 <213> homo sapiens

<400> 36

Gly Gly Ala His Phe Thr Thr Arg Leu Ser Thr Leu Arg  
 1 5 10

<210> 37  
 <211> 13  
 <212> PRT  
 <213> homo sapiens

<400> 37

Thr Thr Arg Leu Ser Thr Leu Arg Cys Tyr Glu Asp Thr  
 1 5 10

<210> 38  
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 <212> PRT  
 <213> homo sapiens

<400> 38

Leu Ala Ala Met Phe Ser Gly Arg His Tyr Ile Pro Thr  
 1 5 10

<210> 39  
 <211> 96  
 <212> PRT  
 <213> homo sapiens

<400> 39

Glu Val Val Pro Leu Asn Ile Gly Gly Ala His Phe Thr Thr Arg Leu  
 1 5 10 15

Ser Thr Leu Arg Cys Tyr Glu Asp Thr Met Leu Ala Ala Met Phe Ser  
 20 25 30

Gly Arg His Tyr Ile Pro Thr Asp Ser Glu Gly Arg Tyr Phe Ile Asp  
 35 40 45

-----Arg-Asp-Gly-Thr-His-Phe-Gly-Asp-Val-Leu-Asn-Phe-Leu-Arg-Ser-Gly-----

50 55 60  
 Asp Leu Pro Pro Arg Glu Arg Val Arg Ala Val Tyr Lys Glu Ala Gln  
 65 70 75 80

Tyr Tyr Ala Ile Gly Pro Leu Leu Glu Gln Leu Glu Asn Met Gln Pro  
 85 90 95

<210> 40  
 <211> 25  
 <212> PRT  
 <213> homo sapiens

<400> 40

Ala Lys Leu Lys Ser Leu Thr Pro Ser Trp Leu Met Ser Val Leu Ile  
 1 5 10 15

Lys Met Pro Pro Gly Val Thr Ser Trp  
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<210> 41  
 <211> 39  
 <212> DNA  
 <213> homo sapiens

<400> 41  
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<210> 42  
 <211> 38  
 <212> DNA  
 <213> homo sapiens

<400> 42  
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<210> 43  
 <211> 49  
 <212> DNA  
 <213> homo sapiens

<400> 43  
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<210> 44  
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 <212> DNA  
 <213> homo sapiens

<400> 44  
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<210> 45  
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 <213> Homo sapiens  
  
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 <210> 47  
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 <210> 48  
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 <212> DNA  
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 <400> 48  
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 <210> 49  
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 <212> DNA  
 <213> Homo sapiens  
  
 <400> 49  
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 <210> 50  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens  
  
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 <210> 51  
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<213> homo sapiens

<400> 51

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<210> 52

<211> 20

<212> DNA

<213> Drosophila melanogaster

<400> 52

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<210> 53

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<212> DNA

<213> Drosophila melanogaster

<400> 53

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<210> 54

<211> 21

<212> DNA

<213> Drosophila melanogaster

<400> 54

actgcagccg attcattaat g 21

<210> 55

<211> 48

<212> DNA

<213> Drosophila melanogaster

<400> 55

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<210> 56

<211> 48

<212> DNA

<213> Drosophila melanogaster

<400> 56

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<210> 57

<211> 21

<212> DNA

<213> Drosophila melanogaster

<400> 57  
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<210> 58  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<400> 58  
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<210> 59  
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 <212> DNA  
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<400> 59  
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<210> 60  
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 <212> DNA  
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<400> 60  
 gaggtgcagc tggcagtc tgg 23

<210> 61  
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<400> 61  
 caggtgcagc tgcaggagtc ggg 23

<210> 62  
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 <212> DNA  
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<400> 62  
 gaggtgcagc tggcagtc tgc 23

<210> 63  
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 <212> DNA  
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<400> 63  
 caggtacagc tgcagcagtc agg 23

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<210> 64  
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 <400> 64  
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 <210> 65  
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 tgaggagacg gtgaccaggg ttcc 24  
  
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145

150

155

160

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